

In the Sequence Listing:

Please insert a paper copy of the sequence listing as new pages 1-49 in the above-mentioned application.



SEQUENCE LISTING

<110> Snutch, Terrance
Baillie, David L.

<120> MAMMALIAN T-TYPE CALCIUM CHANNELS

<130> 38109-20007.21

<140> 09/611,257

<141> 2000-07-06

<150> 09/346,794

<151> 1999-07-02

<150> 09/030,428

<151> 1998-02-25

<150> 60/039,204

<151> 1997-02-28

<160> 49

<170> FastSEQ for Windows Version 4.0

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<213> Artificial Sequence

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<223> oligonucleotide probe for locating calcium channel

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gtgaaagcac agagcttcta ctgg

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<210> 4

<211> 24

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<223> oligonucleotide probe for locating calcium channel

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<210> 7

<211> 24

<212> DNA

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<220>

<223> oligonucleotide probe for locating calcium channel

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<210> 8

<211> 24

<212> DNA

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ab
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<211> 168
<212> DNA
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cttcccagag tgagctcatc cacctcgtca tgcctgactc gacgttca 168

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<211> 98
<212> DNA

<213> Homo sapiens

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<212> DNA

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26
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 Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile
 35 40 45
 Gln Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg
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 Thr His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met
 65 70 75 80
 His Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His
 85 90 95
 Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr
 100 105 110
 Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe
 115 120 125
 Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly
 130 135 140
 Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys
 145 150 155 160
 Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu
 165 170 175
 Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr
 180 185 190
 Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly
 195 200 205
 Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
 210 215 220
 Lys Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu
 225 230 235 240
 Leu Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe
 245 250 255
 Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu
 260 265 270
 Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp
 275 280 285
 Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro
 290 295 300

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Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr	Tyr	Asn	Val	Cys	Arg	Thr	Gly	Ser
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a6
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Leu Arg Gly Ile Val Asp Ser	Lys Tyr Phe Asn Arg Gly Ile Met	Met
805	810	815
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820	825	830
Ala Ser Ala Ala Gln Pro Gly	Arg Ala Cys Gly Arg Gly Gln Asn Pro	
835	840	845
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850	855	860
Ser Pro Gly Gln Gly Val Leu	Ser His Pro Val Thr Pro Pro His Thr	
865	870	875
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885	890	895
Gly Pro Gly Gln Arg Ser Ser	Asp Met Phe Ala Leu Glu Met Ile Leu	
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Lys Leu Ala Ala Phe Gly Leu	Phe Asp Tyr Leu Arg Asn Pro Tyr Asn	
915	920	925
Ile Phe Asp Ser Ile Ile Val	Ile Ile Ser Ile Trp Glu Ile Val Gly	
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Val Leu Lys Leu Val Arg Phe	Met Pro Ala Leu Arg Arg Gln Leu Val	
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Val Leu Met Lys Thr Met Asp	Asn Val Ala Thr Phe Cys Met Leu Leu	
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Met Leu Phe Ile Phe Ile Phe	Ser Ile Leu Gly Met His Ile Phe Gly	
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Cys Lys Phe Ser Leu Arg Thr	Asp Thr Gly Asp Thr Val Pro Asp Arg	
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Ser Gly Asp Pro Lys Leu Cys	Pro Ile Pro Met Thr Pro Asn Gly His	
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ab
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 Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser
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 Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser
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 Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Ser Ile
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 Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg Gly Asp Arg Gly Glu
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 Asp Glu Glu Glu Ile Asp Tyr Val Ser Gly Gly Gly Ala Glu Gly Asp
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 Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly
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 Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp

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Trp Val His His	Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala	Leu Met	
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Ser Leu Phe Val	Leu Ala Ser Lys Asp Gly Trp Val Asn Ile	Met Tyr	
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Asn Gly Leu Asp	Ala Val Ala Val Asp Gln Gln Pro Val Thr	Asn His	
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Asn Pro Trp Met	Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile	Val Ser	
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Phe Phe Val Leu	Asn Met Phe Val Gly Val Val Val Glu Asn Phe	His	
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Lys Cys Arg Gln	His Gln Glu Ala Glu Glu Ala Arg Arg Arg	Glu Glu	
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Lys Arg Leu Arg	Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln	Arg Leu	
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Pro Tyr Tyr Ala	Thr Tyr Cys His Thr Arg Leu Leu Ile His	Ser Met	
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Cys Thr Ser His	Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile	Cys Leu	
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 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
 50 55 60
 Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp

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Arg	Gln	Asp	Leu	Asn	Ala	Ser	Gly	Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr
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Tyr	Asn	Val	Cys	Arg	Thr	Gly	Ser	Ala	Asn	Pro	His	Lys	Gly	Ala	Ile
		130		135		140									
Ser	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Val	Ile	Phe	Gln	Val	Ile
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Thr	Leu	Glu	Gly	Trp	Val	Ala	Ile	Met	Tyr	Tyr	Val	Met	Asp	Ala	Leu
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 <212> PRT
 <213> Rattus

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 Gly Val Gln Leu Trp Ala Gly Leu Arg Asn Arg Cys Phe Leu Glu
 35 40 45
 Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
 50 55 60
 Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp
 65 70 75 80
 Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
 85 90 95
 Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
 100 105 110
 Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
 115 120 125
 Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile

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145	150	155
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Ser Phe Tyr Asn Phe Ile Tyr Phe	Ile Leu Leu Ile Ile	
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 <212> DNA
 <213> Rattus

<400> 23

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26
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Gly Ala Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
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Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
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Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
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Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
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Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
130 135 140
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
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Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys

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Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val
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Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe
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Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn
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Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu
225					230					235					240
Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile
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Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg
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Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu
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Pro	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser
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Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu
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Arg	Gly	Glu	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Ser	Leu	Asp	Tyr	Glu	Thr
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Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn
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Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr
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Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe
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Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe
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Asp	Ser	Glu	Ala	Val	Tyr	Glu	Phe	Thr	Gln	Asp	Ala	Gln	His	Ser	Asp
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Pro	Glu	Glu	Leu	Thr	Asn	Ala	Leu	Glu	Ile	Ser	Asn	Ile	Val	Phe	Thr
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Val	Ile	Ser	Val	Trp	Glu	Ile	Val	Gly	Gln	Gln	Gly	Gly	Gly	Leu	Ser
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Val	Leu	Arg	Thr	Phe	Arg	Leu	Met	Arg	Val	Leu	Lys	Leu	Val	Arg	Phe
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Leu	Pro	Ala	Leu	Gln	Arg	Gln	Leu	Val	Val	Leu	Met	Lys	Thr	Met	Asp
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Ser	Ile	Leu	Gly	Met	His	Leu	Phe	Gly	Cys	Lys	Phe	Ala	Ser	Glu	Arg
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Asp	Gly	Asp	Thr	Leu	Pro	Asp	Arg	Lys	Asn	Phe	Asp	Ser	Leu	Leu	Trp
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Val	Leu	Tyr	Asn	Gly	Met	Ala	Ser	Thr	Ser	Ser	Trp	Ala	Ala	Leu	Tyr
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Phe	Ile	Ala	Leu	Met	Thr	Phe	Gly	Asn	Tyr	Val	Leu	Phe	Asn	Leu	Leu
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Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp		
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His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp		
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Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly		
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Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly		
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Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln		
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Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser		
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Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys		
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His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile		
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Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp		
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Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe		
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Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly		
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Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu		
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Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg		
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Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly		
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Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly		
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Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu		
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Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg		
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Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met		
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Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr		
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Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His		
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Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala		
1525	1530	1535

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cont

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 1570 1575 1580
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 Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
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 1860 1865 1870
 Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
 1875 1880 1885
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 1940 1945 1950
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 1955 1960 1965
 Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala
 1970 1975 1980
 Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser

ab
 Cont

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Glu Val Ser Gly	Pro Ser Cys Pro	Leu Thr Arg Ser	Ser Ser Phe Trp
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Ser Trp Ala Lys	Asp Pro Pro Glu	Thr Arg Ser Ser	Leu Glu Leu Asp
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Thr Glu Leu Ser	Trp Ile Ser Gly	Asp Leu Leu Pro	Ser Ser Gln Glu
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Glu Pro Leu Phe	Pro Arg Asp Leu	Lys Lys Cys Tyr	Ser Val Glu Thr
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Gln Ser Cys Arg	Arg Arg Pro Gly	Phe Trp Leu Asp	Glu Gln Arg Arg
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His Ser Ile Ala	Val Ser Cys Leu	Asp Ser Gly Ser	Gln Pro Arg Leu
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Cys Pro Ser Pro	Ser Ser Leu Gly	Gly Gln Pro Leu	Gly Gly Pro Gly
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26
 ans

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ab
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26
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Cys Gln Lys Val Ile Ala His Lys Met Phe Asp His Val Val Leu Val		1295
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26
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gtagaggtgg ctgccagctc tgggccccca accctacca gcctcaacat cccacccggg 2160
ccctacagct ccatgcacaa gctgctggag acacagagta caggtgcctg cc 2212

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<210> 31
 <211> 644
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Asp Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
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 Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Arg Pro
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 Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
 35 40 45
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
 50 55 60
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
 65 70 75 80
 Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
 85 90 95
 Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
 100 105 110
 Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe

115	120	125
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys		
130	135	140
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val		
145	150	155
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe		
165	170	175
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn		
180	185	190
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu		
195	200	205
Pro Met Leu Gly Asn Val Leu Leu Cys Phe Phe Val Phe Phe Ile		
210	215	220
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg		
225	230	235
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu		
245	250	255
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser		
260	265	270
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu		
275	280	285
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala		
290	295	300
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr		
305	310	315
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn		
325	330	335
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr		
340	345	350
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser		
355	360	365
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe		
370	375	380
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu		
385	390	395
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe		
405	410	415
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys		
420	425	430
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala		
435	440	445
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu		
450	455	460
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser		
465	470	475
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His		
485	490	495
His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu		
500	505	510
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly		
515	520	525
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly		
530	535	540
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp		
545	550	555
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro		
565	570	575

ab
cont

Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640
Thr Gly Ala Cys

<210> 32
<211> 1608
<212> DNA
<213> Homo sapiens

<400> 32
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cggcggttgg gggggcgctc ccggagagcc ccggggcgcc gggacgcgag gcggagcggg 180
ggtccgagct cggcggtgtc cctcccgaga gcccggcggc cgagcgcggc gcggagctgg 240
gtgccgacga ggagcagcgc gtcccgtacc cggccttggc ggccacggtc ttcttctgcc 300
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tgctgcggcc cctccgcgcc atcaaccgcg tgcctagcat gcggatcctg gtcactctgc 720
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agagccgctg gcgcaagaag gtggacccca gtgctgtgca aggccagggt cccgggcacc 1560
gccagcgcg ggagggcagg cacacagcct cgtgaccca cctggtct 1608

<210> 33
<211> 518
<212> PRT
<213> Homo sapiens

<400> 33
Met Thr Glu Gly Ala Arg Ala Ala Asp Glu Val Arg Val Pro Leu Gly
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Ala Pro Pro Pro Gly Pro Ala Ala Leu Val Gly Ala Ser Pro Glu Ser
20 25 30
Pro Gly Ala Pro Gly Arg Glu Ala Glu Arg Gly Ser Glu Leu Gly Val

	35					40					45				
Ser	Pro	Ser	Glu	Ser	Pro	Ala	Ala	Glu	Arg	Gly	Ala	Glu	Leu	Gly	Ala
	50					55					60				
Asp	Glu	Glu	Gln	Arg	Val	Pro	Tyr	Pro	Ala	Leu	Ala	Ala	Thr	Val	Phe
65					70					75					80
Phe	Cys	Leu	Gly	Gln	Thr	Thr	Arg	Pro	Arg	Ser	Trp	Cys	Leu	Arg	Leu
				85					90					95	
Val	Cys	Asn	Pro	Trp	Phe	Glu	His	Val	Ser	Met	Leu	Val	Ile	Met	Leu
			100					105					110		
Asn	Cys	Val	Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Val	Glu	Cys
		115					120					125			
Gly	Ser	Glu	Arg	Cys	Asn	Ile	Leu	Glu	Ala	Phe	Asp	Ala	Phe	Ile	Phe
	130					135					140				
Ala	Phe	Phe	Ala	Val	Glu	Met	Val	Ile	Lys	Met	Val	Ala	Leu	Gly	Leu
145					150					155					160
Phe	Gly	Gln	Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe
				165					170					175	
Phe	Ile	Val	Val	Ala	Gly	Met	Met	Glu	Tyr	Ser	Leu	Asp	Gly	His	Asn
			180					185					190		
Val	Ser	Leu	Ser	Ala	Ile	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg
		195					200					205			
Ala	Ile	Asn	Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu
	210					215					220				
Asp	Thr	Leu	Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val
225					230					235					240
Phe	Phe	Ile	Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu
				245					250					255	
Arg	Asn	Arg	Cys	Phe	Leu	Asp	Ser	Ala	Phe	Val	Arg	Asn	Asn	Asn	Leu
			260					265					270		
Thr	Phe	Leu	Arg	Pro	Tyr	Tyr	Gln	Thr	Glu	Glu	Gly	Glu	Glu	Asn	Pro
		275					280					285			
Phe	Ile	Cys	Ser	Ser	Arg	Arg	Asp	Asn	Gly	Met	Gln	Lys	Cys	Ser	His
	290					295					300				
Ile	Pro	Gly	Arg	Arg	Glu	Leu	Arg	Met	Pro	Cys	Thr	Leu	Gly	Trp	Glu
305					310					315					320
Ala	Tyr	Thr	Gln	Pro	Gln	Ala	Glu	Gly	Val	Gly	Ala	Ala	Arg	Asn	Ala
				325					330					335	
Cys	Ile	Asn	Trp	Asn	Gln	Tyr	Tyr	Asn	Val	Cys	Arg	Ser	Gly	Asp	Ser
		340						345					350		
Asn	Pro	His	Asn	Gly	Ala	Ile	Asn	Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp
		355					360					365			
Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr	Leu	Glu	Gly	Trp	Val	Asp	Ile	Met
	370					375					380				
Tyr	Tyr	Val	Met	Asp	Ala	His	Ser	Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile
385					390					395					

Gly Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala
 500 505 510
 Ser Val His His Leu Val
 515

<210> 34
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 34
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 acagcctcaa gcacaagccg ccgtcggcgg agcatgagtc cctgtctctt gcggagcgcg 180
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 tgcacacccc acacgcccac cacattcatc acgggcccc tctggcgcac cgccaccgcc 300
 accaccgccg gacgtgtcc ctgcacaaca gggactcggg ggacctggcc gagctggtgc 360
 ccgcggtggg cgcacacccc cgggcccgcct ggaggggcggc agggcccggcc cccgggcatg 420
 aggactgcaa tggcaggatg cccagcatcg ccaaagacgt cttcaccaag atgggcgacc 480
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<210> 35
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 35
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 20 25 30
 Ala Ser Arg Arg Ser Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser
 35 40 45
 Ala Glu His Glu Ser Leu Leu Ser Ala Glu Arg Gly Gly Ala Arg
 50 55 60
 Val Cys Glu Val Ala Ala Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu
 65 70 75 80
 His Thr Pro His Ala His His Ile His His Gly Pro His Leu Ala His
 85 90 95
 Arg His Arg His His Arg Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser
 100 105 110
 Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly Ala His Pro Arg Ala
 115 120 125
 Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly
 130 135 140
 Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg

145		150		155		160
Gly Asp Arg Gly Glu Asp Glu Glu Glu Ile Asp Tyr Thr Leu Cys Phe						
	165		170		175	
Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp Trp Cys Glu Val						
	180		185		190	
Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu Asn Arg Phe Arg						
	195		200		205	
Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val						
	210		215		220	
Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro						
	225		230		235	
Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn						
	245		250		255	
Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val						
	260		265		270	
Ser Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp						
	275		280		285	
Asn Val Leu Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val						
	290		295		300	
Val Ser Leu Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg						
	305		310		315	
Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg						
	325		330		335	
Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser Ser Leu Lys						
	340		345		350	
Pro Ile Gly Asn Ile Val Leu						
	355					

<210> 36
 <211> 6892
 <212> DNA
 <213> Homo sapiens

<400> 36
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 acctgtcggg ggccgggggc cggccggggc cggggtcagc agaaaaggac ccgggcagcg 180
 cggactccga ggccggagggg ctgccgtacc cggcgctggc cccgggtggtt ttcttctact 240
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 aaaagtgtta cctgggagac acttggaacc ggcttgactt tttcatcgtc atcgcaggga 540
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tggccttctt	tgtcctgaac	atgtttgtgg	gtgtggtggt	ggagaacttc	cacaagtgtg	4680
ggcagcacca	ggaggaagag	gaggccccgc	ggcgggagga	gaagcgccta	cgaagactgg	4740

ab
comp

agaaaaagag aaggaaagcc cagtgc aaac cttactactc cgactactcc cgcttccggc 4800
 tctctggtcca ccacttgtgc accagccact acctggacct ctatcaca ggtgtcatcg 4860
 ggctgaacgt ggtcaccatg gccatggagc actaccagca gccccagatt ctggatgagg 4920
 ctctgaagat ctgcaactac atcttacttg tcatctttgt cttggagtca gttttcaaac 4980
 ttgtggcctt tggtttccgt cggttcttcc aggacaggtg gaaccagctg gacctggcca 5040
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<210> 37
 <211> 2266
 <212> PRT
 <213> Homo sapiens

<400> 37
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 Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
 20 25 30
 Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
 35 40 45
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
 50 55 60
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
 65 70 75 80
 Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
 85 90 95

Thr	Leu	Gly	Met	Phe	Arg	Pro	Cys	Glu	Asp	Ile	Ala	Cys	Asp	Ser	Gln
			100					105					110		
Arg	Cys	Arg	Ile	Leu	Gln	Ala	Phe	Asp	Asp	Phe	Ile	Phe	Ala	Phe	Phe
			115					120					125		
Ala	Val	Glu	Met	Val	Val	Lys	Met	Val	Ala	Leu	Gly	Ile	Phe	Gly	Lys
			130					135					140		
Lys	Cys	Tyr	Leu	Gly	Asp	Thr	Trp	Asn	Arg	Leu	Asp	Phe	Phe	Ile	Val
			145			150				155					160
Ile	Ala	Gly	Met	Leu	Glu	Tyr	Ser	Leu	Asp	Leu	Gln	Asn	Val	Ser	Phe
				165					170						175
Ser	Ala	Val	Arg	Thr	Val	Arg	Val	Leu	Arg	Pro	Leu	Arg	Ala	Ile	Asn
			180					185						190	
Arg	Val	Pro	Ser	Met	Arg	Ile	Leu	Val	Thr	Leu	Leu	Leu	Asp	Thr	Leu
			195				200						205		
Pro	Met	Leu	Gly	Asn	Val	Leu	Leu	Leu	Cys	Phe	Phe	Val	Phe	Phe	Ile
			210				215						220		
Phe	Gly	Ile	Val	Gly	Val	Gln	Leu	Trp	Ala	Gly	Leu	Leu	Arg	Asn	Arg
					230					235					240
Cys	Phe	Leu	Pro	Glu	Asn	Phe	Ser	Leu	Pro	Leu	Ser	Val	Asp	Leu	Glu
				245					250					255	
Arg	Tyr	Tyr	Gln	Thr	Glu	Asn	Glu	Asp	Glu	Ser	Pro	Phe	Ile	Cys	Ser
			260					265						270	
Gln	Pro	Arg	Glu	Asn	Gly	Met	Arg	Ser	Cys	Arg	Ser	Val	Pro	Thr	Leu
			275				280							285	
Arg	Gly	Asp	Gly	Gly	Gly	Gly	Pro	Pro	Cys	Gly	Leu	Asp	Tyr	Glu	Ala
			290			295					300				
Tyr	Asn	Ser	Ser	Ser	Asn	Thr	Thr	Cys	Val	Asn	Trp	Asn	Gln	Tyr	Tyr
					310					315					320
Thr	Asn	Cys	Ser	Ala	Gly	Glu	His	Asn	Pro	Phe	Lys	Gly	Ala	Ile	Asn
				325					330					335	
Phe	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Ala	Ile	Phe	Gln	Val	Ile	Thr
			340					345					350		
Leu	Glu	Gly	Trp	Val	Asp	Ile	Met	Tyr	Phe	Val	Met	Asp	Ala	His	Ser
			355				360					365			
Phe	Tyr	Asn	Phe	Ile	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Val	Gly	Ser	Phe
			370			375					380				
Phe	Met	Ile	Asn	Leu	Cys	Leu	Val	Val	Ile	Ala	Thr	Gln	Phe	Ser	Glu
					390					395					400
Thr	Lys	Gln	Arg	Glu	Ser	Gln	Leu	Met	Arg	Glu	Gln	Arg	Val	Arg	Phe
				405					410					415	
Leu	Ser	Asn	Ala	Ser	Thr	Leu	Ala	Ser	Phe	Ser	Glu	Pro	Gly	Ser	Cys
			420					425					430		
Tyr	Glu	Glu	Leu	Leu	Lys	Tyr	Leu	Val	Tyr	Ile	Leu	Arg	Lys	Ala	Ala
			435				440					445			
Arg	Arg	Leu	Ala	Gln	Val	Ser	Arg	Ala	Ala	Gly	Val	Arg	Val	Gly	Leu
			450				455					460			
Leu	Ser	Ser	Pro	Ala	Pro	Leu	Gly	Gly	Gln	Glu	Thr	Gln	Pro	Ser	Ser
					470				475						480
Ser	Cys	Ser	Arg	Ser	His	Arg	Arg	Leu	Ser	Val	His	His	Leu	Val	His
				485					490					495	
His	His	His	His	His	His	His	His	Tyr	His	Leu	Gly	Asn	Gly	Thr	Leu
				500				505					510		
Arg	Ala	Pro	Arg	Ala	Ser	Pro	Glu	Ile	Gln	Asp	Arg	Asp	Ala	Asn	Gly
			515				520					525			
Ser	Arg	Arg	Leu	Met	Leu	Pro	Pro	Pro	Ser	Thr	Pro	Ala	Leu	Ser	Gly
			530				535					540			
Ala	Pro	Pro	Gly	Gly	Ala	Glu	Ser	Val	His	Ser	Phe	Tyr	His	Ala	Asp

26
Cont

545 550 555 560
 Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
 565 570 575
 Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
 580 585 590
 Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
 595 600 605
 Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
 610 615 620
 Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
 625 630 635 640
 Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
 645 650 655
 Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
 660 665 670
 Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
 675 680 685
 Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
 690 695 700
 Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
 705 710 715 720
 Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
 725 730 735
 Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
 740 745 750
 Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
 755 760 765
 Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
 770 775 780
 Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
 785 790 795 800
 Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
 805 810 815
 Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
 820 825 830
 Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
 835 840 845
 Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
 850 855 860
 Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
 865 870 875 880
 Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
 885 890 895
 Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
 900 905 910
 Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
 915 920 925
 Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
 930 935 940
 Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
 945 950 955 960
 Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Glu Ile Ser Lys Arg Glu
 965 970 975
 Asp Ala Ser Gly Gln Leu Ser Cys Ile Gln Leu Pro Val Asp Ser Gln
 980 985 990
 Gly Gly Asp Ala Asn Lys Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro
 995 1000 1005

26
 Cnt

Ser Leu Asp Gly Asp Gly Asp Arg Lys Lys Cys Leu Ala Leu Val Ser
 1010 1015 1020
 Leu Gly Glu His Pro Glu Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile
 1025 1030 1035 1040
 Ile His Thr Ala Ala Thr Pro Met Ser Leu Pro Lys Ser Thr Ser Thr
 1045 1050 1055
 Gly Leu Gly Glu Ala Leu Gly Pro Ala Ser Arg Arg Thr Ser Ser Ser
 1060 1065 1070
 Gly Ser Ala Glu Pro Gly Ala Ala His Glu Met Lys Ser Pro Pro Ser
 1075 1080 1085
 Ala Arg Ser Ser Pro His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr
 1090 1095 1100
 Ser Arg Arg Ser Ser Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys
 1105 1110 1115 1120
 Arg Arg Ser Pro Ser Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly
 1125 1130 1135
 Gln Glu Ser Gln Asp Glu Glu Glu Ser Ser Glu Glu Glu Arg Ala Ser
 1140 1145 1150
 Pro Ala Gly Ser Asp His Arg His Arg Gly Ser Leu Glu Arg Glu Ala
 1155 1160 1165
 Lys Ser Ser Phe Asp Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His
 1170 1175 1180
 Arg Thr Ala Ser Gly Arg Gly Ser Ala Ser Glu His Gln Asp Cys Asn
 1185 1190 1195 1200
 Gly Lys Ser Ala Ser Gly Arg Leu Ala Arg Ala Leu Arg Pro Asp Asp
 1205 1210 1215
 Pro Pro Leu Asp Gly Asp Asp Ala Asp Asp Glu Gly Asn Leu Ser Lys
 1220 1225 1230
 Gly Glu Arg Val Arg Ala Trp Ile Arg Ala Arg Leu Pro Ala Cys Tyr
 1235 1240 1245
 Leu Glu Arg Asp Ser Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg
 1250 1255 1260
 Phe Arg Leu Leu Cys His Arg Ile Ile Thr His Lys Met Phe Asp His
 1265 1270 1275 1280
 Val Val Leu Val Ile Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu
 1285 1290 1295
 Arg Pro Lys Ile Asp Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu
 1300 1305 1310
 Ser Asn Tyr Ile Phe Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys
 1315 1320 1325
 Val Val Ala Leu Gly Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser
 1330 1335 1340
 Ser Trp Asn Val Leu Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp
 1345 1350 1355 1360
 Ile Leu Val Ser Met Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met
 1365 1370 1375
 Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile
 1380 1385 1390
 Ser Arg Ala Gln Gly Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser
 1395 1400 1405
 Leu Lys Pro Ile Gly Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile
 1410 1415 1420
 Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val
 1425 1430 1435 1440
 Cys Gln Gly Glu Asp Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala
 1445 1450 1455
 Glu Ala Ser Tyr Arg Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu

26
 Cont

	1460		1465		1470
Gly	Gln	Ala	Leu	Met	Ser
	1475		1480		1485
Val	Asp	Ile	Met	Tyr	Asp
	1490		1495		1500
Pro	Ile	Met	Asn	His	Asn
1505			1510		1515
Leu	Leu	Ile	Val	Ala	Phe
	1525		1530		1535
Val	Glu	Asn	Phe	His	Lys
	1540		1545		1550
Arg	Arg	Arg	Glu	Glu	Lys
	1555		1560		1565
Lys	Ala	Gln	Cys	Lys	Pro
	1570		1575		1580
Leu	Val	His	His	Leu	Cys
1585			1590		1595
Gly	Val	Ile	Gly	Leu	Asn
	1605		1610		1615
Gln	Pro	Gln	Ile	Leu	Asp
	1620		1625		1630
Thr	Val	Ile	Phe	Val	Leu
	1635		1640		1645
Phe	Arg	Arg	Phe	Phe	Gln
	1650		1655		1660
Val	Leu	Leu	Ser	Ile	Met
1665			1670		1675
Ala	Ser	Leu	Pro	Ile	Asn
	1685		1690		1695
Arg	Ile	Ala	Arg	Val	Leu
	1700		1705		1710
Ala	Leu	Leu	Asp	Thr	Val
	1715		1720		1725
Gly	Leu	Leu	Phe	Met	Leu
	1730		1735		1740
Glu	Leu	Phe	Gly	Asp	Leu
1745			1750		1755
Leu	Gly	Arg	His	Ala	Thr
	1765		1770		1775
Leu	Phe	Arg	Val	Ser	Thr
	1780		1785		1790
Thr	Leu	Arg	Asp	Cys	Asp
	1795		1800		1805
Ser	Pro	Ile	Tyr	Phe	Val
	1810		1815		1820
Val	Asn	Val	Val	Ile	Ala
1825			1830		1835
Lys	Glu	Ala	Lys	Glu	Glu
	1845		1850		1855
Met	Lys	Thr	Leu	Ser	Pro
	1860		1865		1870
Leu	Trp	Pro	Gly	Val	Glu
	1875		1880		1885
Gly	Ala	Leu	His	Pro	Ala
	1890		1895		1900
Leu	Glu	His	Pro	Thr	Met
1905			1910		1915
					1920

26
Cont

Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
 1925 1930 1935
 Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro
 1940 1945 1950
 Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val
 1955 1960 1965
 Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu
 1970 1975 1980
 Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro Thr Trp
 1985 1990 1995 2000
 Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
 2005 2010 2015
 Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
 2020 2025 2030
 Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro
 2035 2040 2045
 Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr
 2050 2055 2060
 Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys His Met
 2065 2070 2075 2080
 Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly
 2085 2090 2095
 Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
 2100 2105 2110
 Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Pro Pro Ser
 2115 2120 2125
 Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln
 2130 2135 2140
 Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala
 2145 2150 2155 2160
 Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro
 2165 2170 2175
 Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys
 2180 2185 2190
 Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu Ser Gln
 2195 2200 2205
 Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala
 2210 2215 2220
 Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser
 2225 2230 2235 2240
 Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly
 2245 2250 2255
 Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
 2260 2265

<210> 38
 <211> 44
 <212> PRT
 <213> C. elegans

<400> 38
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 1 5 10 15
 Glu Gly Trp Thr Asp Phe Glu Thr Leu Ser Phe Lys Gly Trp Asn Val
 20 25 30
 Ile Arg Cys Leu Thr Gly Glu Asp Trp Asn Asp Ile

35

40

<210> 39
 <211> 44
 <212> PRT
 <213> C. elegans

<400> 39
 Leu Ala Ala Ser Gln Glu Gly Trp Val Tyr Val Gln Ile Ile Thr Gln
 1 5 10 15
 Glu Gly Trp Thr Asp Val Glu Thr Leu Ser Tyr Lys Gly Trp Asn Val
 20 25 30
 Val Arg Ser Val Thr Gly Glu Asp Trp Asn Asp Ile
 35 40

<210> 40
 <211> 44
 <212> PRT
 <213> Rattus

<400> 40
 Glu Ala Ser Ser Gln Glu Gly Trp Val Phe Leu Gln Ile Leu Thr Gln
 1 5 10 15
 Glu Gly Trp Val Asp Val Glu Val Leu Ser Leu Lys Gly Trp Val Glu
 20 25 30
 Val Arg Ile Val Thr Gly Glu Asp Trp Asn Lys Ile
 35 40

<210> 41
 <211> 44
 <212> PRT
 <213> Unknown

<220>
 <223> Mammalian L-Type Ca Channel

<400> 41
 Gln Cys Ile Thr Met Glu Gly Trp Thr Asp Val Gln Ile Leu Thr Gly
 1 5 10 15
 Glu Asp Trp Asn Ser Val Thr Val Ser Thr Phe Glu Gly Trp Pro Glu
 20 25 30
 Leu Arg Cys Ala Thr Gly Glu Ala Trp Gln Asp Ile
 35 40

<210> 42
 <211> 44
 <212> PRT
 <213> Unknown

<220>
 <223> Mammalian T-Type Ca Channel

<400> 42

Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Gln Ile Leu Thr Gln
 1 5 10 15
 Glu Asp Trp Asn Lys Val Val Leu Ala Ser Lys Asp Gly Trp Val Asp
 20 25 30
 Ile Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile
 35 40

<210> 43
 <211> 44
 <212> PRT
 <213> Unknown

<220>
 <223> Mammalian Na Channels

<400> 43
 Arg Leu Met Thr Gln Asp Phe Trp Glu Asn Leu Arg Val Leu Cys Gly
 1 5 10 15
 Glu Trp Ile Glu Thr Met Gln Val Ala Thr Phe Lys Gly Trp Met Asp
 20 25 30
 Ile Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu
 35 40

<210> 44
 <211> 9
 <212> PRT
 <213> Unknown

<220>
 <223> Consensus motif

<400> 44
 Gln Gln Glu Leu Gly Tyr Trp Ile Glu
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<210> 45
 <211> 4
 <212> PRT
 <213> Unknown

<220>
 <223> T-type channels in P-regions of domains I-IV

<400> 45
 Glu Glu Asp Asp
 1

<210> 46
 <211> 4
 <212> PRT
 <213> Unknown

<220>
<223> Na channels in the P-region of domains I-IV

<400> 46
Asp Glu Lys Ala
1

<210> 47
<211> 4
<212> PRT
<213> Unknown

<220>
<223> L-type calcium channels in P-regions of domains
I-IV

<400> 47
Glu Glu Glu Glu
1

<210> 48
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

ab
<400> 48
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18

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
gcacccagtg gagaaaggtg

20